

1/34

Figure 1

```

>sp|P47901|V1BR_HUMAN VASOPRESSIN V1B RECEPTOR (AVPR V1B) (VASOPRESSIN V3
RECEPTOR) (AVPR V3) (ANTIDIURETIC HORMONE RECEPTOR 1B).
Length = 424

Score = 316 (111.2 bits), Expect = 3.7e-41, Sum P(2) = 3.7e-41
Identities = 70/194 (36%), Positives = 115/194 (59%)

Query:   56 LWLVFVFTIVGNSVLFSTWRR-KKKSRRMTFFVTQLAITDSFTGLVNILTDINWRFTGDF 114
          L + V  GN VL + + +K+SRM FV LA+TD  L +L + W T F
Sbjct:   41 LATVLVLATGGNLAVLLTLGQLGRKRSRMHLFVLHLALD LAVALFQVLPQLLDITYRF 100

Query:   115 TAPDLVCRVVRYLQVLLYASTYVLVSLSIDRYHAIVYPMKFLQGEKQARVLIVIA-WSL 173
          PDL+CR V+YLQV+ ++ASTY+L+++++DRY A+ +P++ LQ  Q+ L++ A W L
Sbjct:   101 QGPDLLCRAVKYLQVLSMFASTYMLLAMTLD RYLA VCHPLRSLQQPGQSTYLLIAAPWLL 160

Query:   174 SFLFSIPTLIIFGKRTL--SNGEVQCWALWPDDSY-WTP--YMTIVAFVLYFIPLTIISI 228
          + +FS+P + IF R + +G + CWA D + W P Y+T  ++ +P+T+++
Sbjct:   161 AAIFSLPQVFIFSLREVIQSGVLDCA---DFGFPWGP RAYLTWTTLAIFVLPVTMLTA 217

Query:   229 MYGIVIRTIW--IKSKT 243
          Y ++ I  +K KT
Sbjct:   218 CYSLICHEICKNLKVKT 234

Score = 131 (46.1 bits), Expect = 3.7e-41, Sum P(2) = 3.7e-41
Identities = 33/80 (41%), Positives = 47/80 (58%)

Query:   258 SSYNRGLISKAKIAIKYSIIILAFICWSPYF---LFDILDNFNLLPDTQERFYASVI 314
          SS N  IS+AKI+ +K + +I+LA+I CW+P+F  ++ + D N PD  A I
Sbjct:   267 SSINT--ISRAKIRTVKMTFVIVLAYIACWAPFFSVQMWSVWDK-NA-PDEDSTNVAFTI 322

Query:   315 IQNLPALNSAINPLIYCVFSSSI 337
          L LNS NP IY F+S +
Sbjct:   323 SMLLGNLNSCCNPWIYMGFNSHL 345

```

Figure 2

```

>sp|P31388|5H6_RAT 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)
(ST-B17).
Length = 436

Score = 224 (78.9 bits), Expect = 6.7e-17, P = 6.7e-17
Identities = 84/309 (27%), Positives = 144/309 (46%)

Query:      3  PGEA--LLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLGLHLLAALDM 60
             PG + + A L V+++ A ++ L++L C A LR S LV+L L++ + M
Sbjct:     23  PGSGGWAAALCVVIVLTAAANSLIVLICTQPA-LRN-TSNFFLVSLFTSDLMVGLVVM 80

Query:     61  PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRIR- 119
             P +L + GR A G C + D S + L++ +S D++L + PLRY R+
Sbjct:     81  PPAMLNALYGRWVLARGLCLLWTAFDVMCCSASIINLCLISLDRYLLISPLRYKLMTA 140

Query:     120 PRYAGLLLGAMGQSALFSGAALGCSWLGYSSAFASCSRLRPPEPERPFRA--FTATL 176
             PR L+LG AW SLA AL S+L + P P + R A F
Sbjct:     141 PRALALILG-AW--SLA---ALA-SFLPLLLGWHELKGKARTPAPGQCRLLASLPFVLVA 192

Query:     177 HAVGFVLPLAVLCLTSLQVHRVARRHCQRMDTVT-----MKALALLADLHPSVR---- 225
             V F LP +C T ++ AR+ ++ +T ++ L + P +
Sbjct:     193 SGVTFFLPSGAICFTYCRILLAARKQAVQVASLTTGTAGQAELETLPVPRTPRPGMESADS 252

Query:     226 QRCLIQKRRRRHRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWILSKCLTYS 285
             +R + R+ +A+ +GI + F + + P+ + +A+ V + +L+ L Y
Sbjct:     253 RRLATKHSRKALKASLTGLGILLGMFFVTWLPFFVANIAQAVCDCISPLFDVLT-WLGYC 311

Query:     286 KAVADPFYTSLLRRPFRQVL 305
             + +P Y L R F++ L
Sbjct:     312 NSTMNPPIIYPLFMRDFKRAL 331

```

Figure 3

>sp|P56479|GALR_MOUSE GALANIN RECEPTOR TYPE 1 (GAL1-R) (GALR1).
Length = 348

Score = 269 (94.7 bits), Expect = $7.9e-24$, P = $7.9e-24$

Identities = 82/289 (28%), Positives = 136/289 (47%)

```

Query:   49 VGFVGNLCVIGILLHNAWKGP-SMIHSLILNLSLADLSLLFSAPIRATAYSKSVWDLG 107
          +G +GN VI +L + GKP S + IILNS+ADL+ LLF P +AT Y+ W LG
Sbjct:   46 MGVLGNSLVITVLARSK-PGKPRSTTNLFILNLSIADLAYLLFCIPFQATVYALPTWVLG 104

Query:  108 WFVCKSSDWFIHTCMAAKSLTIVVVA--KVCIFYASDPAKQVSIHNYTIWSVLVAIWTV 165
          F+CK +F M T+ ++ + + S + ++ + V IW ++
Sbjct:  105 AFICKFIHYFFTVSMLVSIFTLAAMSVDRYVAIVHSRRSSSLRVSRNALLGVGF-IWALS 163

Query:  166 SLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFMSMGKLYPL--LAFG--LPLFFASF 220
          + P + + H + + C P + K Y + FG LPL F
Sbjct:  164 IAMASPVAYHQRLFHRDSNQTFCWEQWPN-----KLHKKAYVCTFVFGYLLPLLLICF 217

Query:  221 YFWRAYDQCKKRGTKTQNLNRQIRSKQVTVMLLSIAIISAVLWLPWVAVLWVWHLKAAG 280
          + + + K+ K + +++ K+ +L + ++ + WLP V LW A
Sbjct:  218 CYAKVLNHLHKK-LKNMSKKSEASKKTAQTVLWVVVVFGISWLPVHVHLWAEF--GAF 274

Query:  281 PAPPQGF--ALSQVLMFSSISANPLIFLVMSEEFREGLKGVWKMMITKKPPTVSESEQ 337
          P P F + L +S SS NP+I+ +SE FR+ K V+K + + P SE++E
Sbjct:  275 PLTPASFFFRIITAHCLAYSNSSVNPPIIYAFLSENFRKAYKQVFKCHVCDSPR-SETKE 332

```

Figure 4

```

>sp:NY2R_BOVIN-NEUROPEPTIDE Y RECEPTOR TYPE 2 (NPY2-R).
      Length = 384

Score = 153 bits (383), Expect = 5e-37
Identities = 93/308 (30%), Positives = 164/308 (53%), Gaps = 7/308 (2%)

Query: 47  DEDEDVTNSRTFFAAKIVIGMALVGIMLVCGIGNFIFIAALVRYKKLRNLTNLLIANLAI 106
           D + ++ +S      ++V+ +A  I+L+  IGN + I  +++K +R +TN  IANLA+
Sbjct: 38  DSEPELIDSTKLIEVQVVLILAYCSIIILGVIGNSLVIHVVIKFKSMRTVTNFFIANLAV 97

Query: 107 SDFLVAIVCCPFEMDYVVVRQLSWEHGHVLCTSVNYLRTVSLYVSTNALLAIAIDRYLAI 166
           +D LV  +C PF + Y ++ +  W+ G VLC  V Y + +++ VST  L  IA+DR+  I
Sbjct: 98  ADLLVNTLCLPFTLTYYLMGE--WKMGPVLCPLVYQAQGLAVQVSTITLTIVIALDRHRCI 155

Query: 167 VHPLRPRMKCQTATGLIALVWTVSILIAIPSAFYTTETVLVIVKSQEKIFCGQIWPVDQQ 226
           V+ L  ++ Q +  +I L W VS L+A P A F  +++ I+  E + C + WP +++
Sbjct: 156 VYHLESKISKQISFLIIGLAWGVSALLASPLAIFREYSLIEIIPDFEIVACTEKWPGEK 215

Query: 227 -LYYKSYFLFIFGIEFVGPPVMTLCYARISRELWFKAVPGFQTEQIRKRLCRRKTVLV 285
           +Y  Y L  I +V P+ ++ Y RI  +L  PG  +  +R  R+KT  +
Sbjct: 216 GIYGTIYSLSSLLILYVLPGLIISFSYTRIWSKLNKHWSPGAADHYHQH---RQKTTKM 272

Query: 286 LMCILTAYVLCWAPFYGFITVRDFFPTVFVKEKHYLTAFYIVECIAMSNMINTLCFVTV 345
           L+C++  ++ W P + F +  D  V + K Y  F +  IAM ++ N L +  +
Sbjct: 273 LVCVVVFAVSWLPLHAFQLAVIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 331

Query: 346 KNDTVKYF 353
           ++ K F
Sbjct: 332 NSNYRKAF 339

```

5/34

Figure 5

```
>sp|P97926|OXYR_MOUSE OXYTOCIN RECEPTOR (OT-R).
```

```
Length = 388
```

```
Score = 164 (57.7 bits), Expect = 8.9e-22, Sum P(2) = 8.9e-22
```

```
Identities = 57/166 (34%), Positives = 84/166 (50%)
```

```
Query: 24 WGLNLT LGGAP-----ASGPPSR-----RVRLVFLGVILVAVAGNTTVLCRLCGGG 71
      W + L LG G P +GPP R RV + L +IL +A++GN VL L
Sbjct: 9 WSIELDLGSGVPPGAEGNLTAGPPRRNEALARVEVAVLCLILFLALSGNACVLLAL---- 64
```

```
Query: 72 GPWAGPKRRKMDFLLVQLALADLYACGGTALSQLAWELLGEPRATGDACRFLQLLOAS 131
      K ++ F + L++ADL L QL W++ R DL CR ++ LQ
Sbjct: 65 -RTTRHKHSRLFFFMKHL SIADLVVAVFQVLPQLLDITF--RFYGPDLCLRLVKYQVV 121
```

```
Query: 132 GRGASAHVLVLIALERRRRAVRLPHGRPLPARA--LAALG-WLLALLLALPPAFV 182
      G AS +L++L++L+R A+ P R L R LA L WL L+ ++P +
Sbjct: 122 GMFASTYLLLLMSLDRCLAICQPL-RSLRRRTDRLAVLATWLGCLVASVPQVHI 174
```

```
Score = 155 (54.6 bits), Expect = 8.9e-22, Sum P(2) = 8.9e-22
```

```
Identities = 49/161 (30%), Positives = 85/161 (52%)
```

```
Query: 217 CHGIFAPLPRWHLQVYAFYEAVAGFVAPVTVLGVACGHLLS--VWV--RHRPQAPAAAA 272
      C +F + W + Y + +A ++ PV VL AC L+S +W R + A AAAA
Sbjct: 187 CWAVF--IQPWGPKAYVTWITLAVYIVPVIVLA-ACYGLISFKIWQNRLKTAIAAAAAAE 243
```

```
Query: 273 WSASPG-----RAPAPSALPRAKVQSLKMSLLALLFVGCELPYFAARLAAAWS-SG 323
      S + G R + + +AK+++KM+ ++ L F+ C P+F ++ + W +
Sbjct: 244 GSDAAGGAGRAALARVSSVKLISKAKIRTVMKTFIIVLAFIVCWTPTFFVQMWVSVDVNA 303
```

```
Query: 324 PAGDWEGEGLSAAALRVVAMANSALNPFVYLFQAGDCRLRRLKRLGSLCCA 376
      P E A+ ++A NS NP++Y+ F L +L +R LCC+
Sbjct: 304 PK---EASAFIIAM-LLASLNSCCNPWIYMLFTG---HLFHELVRQF--LCCS 347
```

Figure 6

```

>sp|Q91178|GPRX_ORYLA PROBABLE G PROTEIN-COUPLED RECEPTOR (FRAGMENT).
Length = 428

Score = 823 (289.7 bits), Expect = 9.8e-83, P = 9.8e-83
Identities = 182/422 (43%), Positives = 266/422 (63%)

Query:   2  ESSPIQSSGNSSTLGRVPQTGPSTASGVPEVGL----RDVASESVALLFMLLDLTAV 57
          ++SP+  S  + S          P P+      P+VG+  +  +  LF M+ L+L A+
Sbjct:   5  KTSPIITSDHSISNFTSLGFGPHPTVP---PDVGVVTSQSQMKDLFGLCFMTVLNLIAL 61

Query:  58  AGNAAVMAVIAKTPALRKVFVFHLCVLDLLAALTMLPLAMLSSSALFDHALFGEVACRL 117
          N  VM  IA+ P L+KF FV HLC VD+L A+ LMPL ++SSS F  +F  + C++
Sbjct:  62  LANTGVMVAIARAPHLKKFAFVCHLCAVDVLCAILLMPLGISSSPFFGTGVFTILECQV 121

Query:  118 YLFLSVCFVSLAILSVSAINVERYYYVHPMRYEVRMTLGLVASVLGVVWKALAMASVP 177
          Y+FL+V + L+IL+++AI+VERY+Y+VHPMRYEV+MT+ LV V++ +W K+L +A V
Sbjct:  122 YIFLNVFLIWLISLITITAIISVERYFYIVHPMRYEVKMTINLVIGVMLLIWFKSLLLALVT 181

Query:  178 VLGRVSWEEGAPSVPPGCSLQWSHSAQCFLFVVVFVAVLYFLLPLLLILVVYCSMFRVARV 237
          + G  +  +      CSL SHS  +F V+F V+ FL P+++I VY ++++VAR
Sbjct:  182 LFGWPPYGHQSSIAASHCSLHASHSRLRGVFAVLCVICFLAPVVVIFSVSAYYKVAR 241

Query:  238 AAMQHGP-LPTWME-TP-RQRSESLSSRSTMTVSSGAPQT-TPHRTFGGGKAADVLLAVG 293
          AA+Q P +PTW + +P + RS+S++S++T++T+ PQ +P R F GGGKAA+ L +
Sbjct:  242 AALQQVPAVPTWADASPAKDRSDSINSQTIIITRTLPQLRSPERAFSGGKAALTIAFV 301

Query:  294 GQFLLCWLPHYFSFHLVVALSAQPISTGQVESVVTWIGYFCFTSNPFFYGCLNRQIRGELS 353
          GQFL+CWL P+F FHL ++L+ S G +E V W+ Y F NP FYG LNRQIR EL
Sbjct:  302 GQFLVCWLPFFIFHLQMSLTGSMKSPGDLEAVNWLAYSSFAVNP SFYGLLNRQIRDELV 361

Query:  354 K-QVCFCKPAPEEELRLPSREGSIEENFLQFLQGTGCPSESWSRPLSPKQ-EPPAVD 411
          K + C +P E+ S EGS +ENFLQF+Q T SE+ S +P+ E A
Sbjct:  362 KFRCCVTQPV---EIGPSSLEGSFQENFLQFIQRTSSSSETHPSFANSNPRNMENQA-- 416

Query:  412 FRIPGQIAEE 421
          +IPGQIEE
Sbjct:  417 HKIPGQIEE 426

```

Figure 7

```

>sp|P23749|RTA_RAT PROBABLE G PROTEIN-COUPLED RECEPTOR RTA.
      Length = 343

Score = 461 (162.3 bits), Expect = 2.3e-44, P = 2.3e-44
Identities = 121/323 (37%), Positives = 178/323 (55%)

Query:   2 NQTLNSSGTVESALNYSRGS-TVHT-AYL----VLSSLAMFTCLCGMAGNSMVIWLLGFR 55
          NQ      G E+  YSRG T+  A L   V + + + CLCG+ GN +V+W GF
Sbjct:  13 NQNMCPGMSEALELYSRGFLTIEQIATLPPPAVTNYIFLLCLCGLVGNGLVWFFGFS 72

Query:   56 MHRNPFICIYILNLAADLLFLFSMASTLSLETQPLVNT-TDKVHELMKRLMYFAYTVGLS 114
          + R PF IY L+LA+AD ++LFS A   L   ++ D V + + +   + G+S
Sbjct:  73 IKRTPFSIYFLHASADGIYLFASKAVIALLNMGTFLGSPDYVRRVSRIVGLCTFFAGVS 132

Query:   115 LLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMGLTSSSFCSKFL--KFNE 172
          LL AIS +RC+SV+FP+W+  RP+ LSA VC LLW L L+  + + FC FL  + +
Sbjct:  133 LLPAISIERCVSVIFPMWYVRRRPKRLSAGVCALLWLLSFLVTSIHNYFCM-FLGHEASG 191

Query:   173 DRCFRVDMVQAALIMGVLTVPMTLSSLTLFVWVRRSSQWRRQPTRLFVVVLASVLVFLI 232
          C +D+  L+  + P+M L L L + V   +++ R++  +L  VVLA V VFL+
Sbjct:  192 TACLNMDSLGILLFFLCPLMVLPLCALILHVECRARR-QRQSAKLNHVLAIVSVFLV 250

Query:   233 CSLPLSIYWFVLYWL-SLPPEMQVLCFSLRSLSSSVSSSANPVYIFLVGSRSHRLPTRS 291
          S+ L I WF L+W+  +P      ++ L  ++SSA P++YFL G +S RL
Sbjct:  251 SSIYLGIDWF-LFWVFQIPAPFPEY---VTDLCICINSSAKPIVYFLAGROKSQRL-WEP 305

Query:   292 LGTVLQQALRE---EPELEGGETPTVGTNEM 319
          L V Q+ALR+ EP      TP   T EM
Sbjct:  306 LRVVFQRALRDGAEPGDAASSTPNTVTMEM 335

```

8/34

Figure 8

```

>sp|Q98907|P2Y3_CHICK P2Y PURINOCEPTOR 3 (P2Y3) (NUCLEOSIDE DIPHOSPHATE
  RECEPTOR).
  Length = 328

Score = 452 (159.1 bits), Expect = 2.0e-43, P = 2.0e-43
Identities = 85/185 (45%), Positives = 116/185 (62%)

Query:   15 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL 74
          C F E++KQV L L YS++F+LGLPLN V+ W K + T Y++NL +ADLLYV
Sbjct:   13 CTFHEEFKQVLLPLVYSVVFLGLPLNAVVGQIWLARKALTRTTIYMLNLAMADLLYVC 72

Query:   75 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCTISVHQFLGVCHPLCSLPY 133
          LP LI Y+ D WPGF+ CK V F FY NL+GSIL LTCISV +++G+CHPL S
Sbjct:   73 SLPLLIYNYTQKDYWPGDFTCKFVRQFYTNLHGSILFLTCTISVQRYMGICHPLASWHK 132

Query:   134 RT-RRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWDMTSQENFDRLFAYGIVLT 192
          + ++ WL + W +V+ Q LPT F+ T ++ YD++ + F YGI LT
Sbjct:   133 KKGKLTWLCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPDRSTSYFPYGITLT 192

Query:   193 LSGFL 197
          ++GFL
Sbjct:   193 ITGFL 197

```


Figure 9

```

>sp|002824|A1AA RABIT ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A-ADRENOCEPTOR)
      (ALPHA-1C ADRENERGIC RECEPTOR).
      Length = 466

Score = 295 (103.8 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31
Identities = 66/215 (30%), Positives = 113/215 (52%)

Query:   8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
          S S+SS+ P + P++++ I+ +L + +GNI++ L + L VT+
Sbjct:   5 SGNASDSSNCTHPPA--PVNISKAILLGVLGLILFVGLGNILVILSVACHRHLSVTH 62

Query:  68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFASFVNTIVVVSV 127
          +I NL V DLL S V P+ + +W FC ++ L AS+ ++ V+S+
Sbjct:  63 YYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVISI 122

Query:  128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWQAAFDERNALCSMIWG 187
          DRY+ + +PL YP+ +TQRRG L W +++ S PL+GW Q A D+ +C +
Sbjct:  123 DRYIGVSYPLRYPTIVTQRRGLRALLCVAFSLVISVGLFVGWRQPAPDDET-ICQI--N 179

Query:  188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ 222
          P Y + S + +PL +++A Y V+ A+R+
Sbjct:  180 EEPGYVLFSAIGSFYVPLTIILAMYCRVYVAKRE 214

Score = 106 (37.3 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31
Identities = 23/75 (30%), Positives = 41/75 (54%)

Query:  396 KAAKVIFIIIFSIVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWFLFQCCIHYPVYG 455
          KAAK + I++ +VL P+ + + + + + P+ V I+ WL +L CI+P +Y
Sbjct:  269 KAAKTGLIVGFCVLCWLPFFLVMPIGSFFP-DFKPPETVKFIVFWLGLYNLNCINPIIYP 327

Query:  456 YMHKTIKKEIQDMLK 470
          + KK Q++LK
Sbjct:  328 CSSQEKKAFQNVLK 342

```

10/34

Figure 10

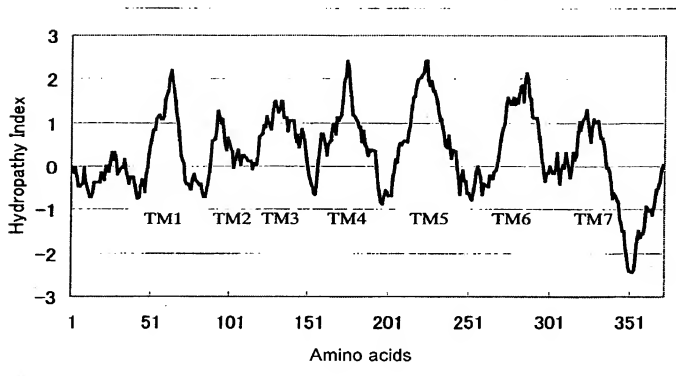


Figure 11

```

X64878      MEGALAAAN---WSA-EAA-NASAAPPGAEG-----NRTAGPPRRNEALARVEAVLCLIL
U82440      MEGELAAAN---WST-EAV-NSSAAPPGAEG-----NCTAGPPRRNEALARVEAVLCLIL
X93313      MEGCLCLN---DCS-ELP-NSSWVNSSMEMQHSSNDTROPKRNKEEVAKVETVLALIL
X87783      MEEMFKEQDF-WSFNESSRNTVCGNETFGG-----NQTVPFLKRNEEVAKVETVLALVL
AF184966    -----MEKPGNITLHP-----NGSDPFRGNEEVAQIEIMVLISITF
X76321      -----MGRIANQTTS-----NDTDPFRGNEEVAKMEIITLVSYTF
AF147743    MKNFSFPMQD-STHQTESPPHRLSLTNKS-----DPVGRPERDEQLAQVEI AVLGVIF
GPRv8      MPANFTEGSDSGTGQTLDSSPVACTETVTFTEVGEKNGSFYYSFKTEQLITLVWLF
AE003754    -----MKCDHTLGFQTEQFAVLWILF

      . . . . .

TM1 #####      ##### TM2 #####

LLALSGNACVLLALRTTRQKHSRLFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGPDL
U82440      LLALSGNACVLLALRTTRQKHSRLFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGPDL
X93313      FLALAGNICVLLGIIYIRHKHSRYFFMKHLSIADLVVAVFQVLPQLIWDITFRFYAPDL
X87783      FLALAGNLCVLIAYITAKHTQSRMYLWKHLSIADLVVAVFQVLPQLIWDITFRFYGPDL
AF184966    FVAVI GNVSVLLAMHTYTKKMSRMHLFIKHLSLADLVVAVFQVLPQLCWEITYRFFGPDF
X76321      FVAVI GNLSVLLAMHTYTKKMSRMHLFIKHLSLADLVVAVFQVLPQLCWEITYRFFGPDF
AF147743    LTVASGNFILIILVLRKKKLSRMVYFVLHLSIADLVVAVFQVLPQLIWDITGVDFGPDF
GPRv8      VFTI VGNVSVLFTSWR-RRKLSRMTYFVTLQAI TDSFTGLVNIIDINWRFTGDFTAPDL
AE003754    TVI VLGNSAVL FVMFINKNRKSRMYNFIKQLALADLCVGLLNVLTDI IWRITISWRAGNL

**   . . .   . . .   . . .   . . .   . . .   . . .   . . .   . . .   . . .

      @##### TM3 #####      ##### TM4 #

LCRLVKYLQVVGMAFASTYLLLLMSLDRCLAICQPLRSLSRRRT---DRLAVLATWLGCLVAS
U82440      LCRLVKYLQVVGMAFASTYLLLLMSLDRCLAICQPLRSLSRRRT---DRLAVLATWLGCLVAS
X93313      VCRVLVYTLQVVGMAFASTYMLLLNSLDRCLAICQPLRSLSRRS---DCVYVLFTWILSFLLS
X87783      LCRLVKYLQVVGMAFASTYMLVLMISDRCLAICQPLRSLSHKKR---DRCVYI VSNWLSLVS
AF184966    LCRI VKHLQVLTGMFASTYVMVMWMTLDRIAYI CHPLKTLQQPQTSYIMIVSTWMSCLVFS
X76321      LCRI VKHLQVLTGMFASTYVMVMWMTLDRIAYI ICHPLKTLQQPQTRAYIMIGSTWMLCSLFS
AF147743    LCRI I KYTLQGLMGFASTYMI VVMTVDRYQAVCYPMVTFQKKRALWNIPICTSWSILIS
GPRv8      VCRVYVYLQVLLVSTYVLVLSIDRYTHAI VYPMKFLQGEKQ-ARVLI VAWNSLFLFS
AE003754    ACKAIRFSQVCVTYSSTYVLVAMSIDRYDAI THPMFNFSKSWKR-ARHLVAGAWLISALFS

      . . .   . . .   . . .   . . .   . . .   . . .   . . .   . . .   . . .

#####      @      ##### TM5 #####

APQVHIFSLREVADG---VFDCWAVFIQP---WGPKAYITWITLAVYIPVIVLATCYGLS
U82440      APQVHIFSLREVADG---VFDCWAVFIQP---WGPKAYITWITLAVYIPVIVLAACYGLS
X93313      TPQTVIFSLTREYVNG---VYDCRADFIQP---WGPKAYITWITLAVYIIPVIMVSLCYGLS
X87783      VPQVYIFSLREI GNG---VYDCWGVDFIQP---WGAKAYITWITSLTIYIIPVAILGVCYGLS
AF184966    TPQVYIFSLSEVKNGSTVYDCWHAFFIEP---WGARAYITWITGGIIFLVPVIVLVNCCYGLS
X76321      TPQVYIFSLSEIQNGSYVYDCWGHFIEP---WGIIRAYITWITVGIFLIPVILMICYGFI
AF147743    LPQVFI FSKIEI SPG---IFECWAEFIQP---WGRPAYITWITVLVIFIPSTITICQVYGI
GPRv8      IPTLI I QFKRTLNG---EQVCAWLPWDSYWTPT---YMTI VAVL VYFIPSTIISIMYGI
AE003754    LPI LVLYEELIQGH---PQCWIELGSPAIQWV---YMSLVSATLFAIPALII SACYAIV

      *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

```

Figure 12

[illegible]

13/34

Figure 13

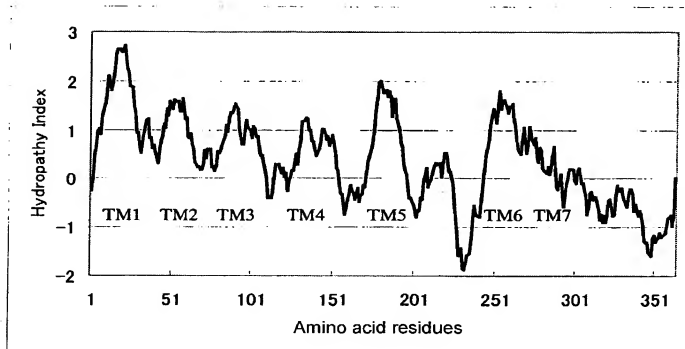


Figure 14

```

***** TM1 *****
GPRv12_ORF      MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLGLHLLAALDM
AF208288        MNSWDAGLAGLLVGTIGVSLLSNGLVLLCLLHSAIDRRQAPALFTLNLTCGNLLCTVVNM
                *.. *? ***** ..*:*:**** ***** :*:*:* *..* :*: *:* *..*

*****          @***** TM3 *****
GPRv12_ORF      PFTLLGVMRGRTPSAPGACQVIGFLOTFLASNAALSVAALSADQNLVAGVFLPYACRLRP
AF208288        PLTLAGVVAQRQPGADRLCRLAAFLDTFLAANSMLSMAALSIDRWAVVVFPLSYRAKMRL
                *:* *:* * *.. *:* :*****:* *:*:**** *:*:* * * *..*

***** TM4 *****          @          *****
GPRv12_ORF      RYAGLLGCAWQCSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAATATLHAVG
AF208288        RDAAFMVAYTWLHALTFPATALALSWLGHFQLYASCTLCRRPDERLRFVAFVTSFAHLS
                *..*..* *..*:*:*:*..*..* *..* *..* *..* *..* *..*

TM5 *****
GPRv12_ORF      FVLPLAVLCLTSLQVHRVARRHCQRMDVTMKALALLADLHPSVRQRCLIQKRRRRHRT
AF208288        FLLSFI VLCFTYLKVLKVARFHCKRI DVI TMQTLVLLVDIHPSVRECL EEQKRRQRAT
                *..*..* *..* *..* *..*:*:*:*..*..* *..* *..* *..* *..*

***** TM6 *****          ***** TM7 *****
GPRv12_ORF      RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFYTSLLRRP
AF208288        KKISTF IGTFVLCFAPYVITRLVELFSTAPIDSHWGLVSKCLAYSKAASDPFVYSLLRHQ
                :*.. *..* *..* *..* *..* *..* *..* *..* *..* *..* *..*

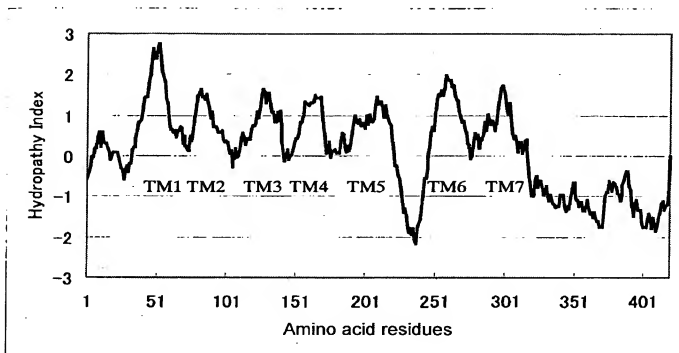
GPRv12_ORF      FRQVLAGMWHRLKRTPRPASTHDSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
AF208288        YRRSCKELLNRI RNR-----S IHSVGLTGD SHSQNI LPYSE-----
                *:* :*:*:*:* *..*..* *..*..*

GPRv12_ORF      QTH
AF208288        ---

```

15/34

Figure 15



16/34

Figure 16

```

*****
##### TM1 #####
1 MLAAAFADSN SSSMNVSAH LHFAGGYLPS DSQDWRTIIP ALLVAVCLVG FVGNLCVIGI 60

*****
##### TM2 #####
61 LLHNAWKGP SMIHSLILNL SLADLSLLF SAPIRATAYS KSVWDLGWV CKSSDWFIHT 120

*****
##### TM3 #####
##### TM4 #####
121 CMAAKSLTIV VVAKVCFMYA SDPAKQVSIH NYTIWSVLVA IWTVASLLPL PEWFFSTIRH 180

*****
##### TM5 #####
181 HEGVEMCLVD VPAVAEFMS MFGKLYPLA FGLPLFFASF YFWRAYDQCK KRGTKQNLR 240

*****
##### TM6 #####
##### TM7 #####
241 NQIRSKQTV MLLSIAIISA VLWLPEWVAV LWVWHLKAAG PAPPQGFIAL SQVLMFSISS 300

*****
#####
301 ANPLIFLYMS EEFREGLKGV WKWMITKPP TVSESQETPA GNSEGLPKV PSPSPASIP 360

361 EKEKPSSPS GKGKTEKAEI PILPDVEQFW HERDTVPSVQ ONDPIWEHE DQETGEGVK 419

```


17/34

Figure 17

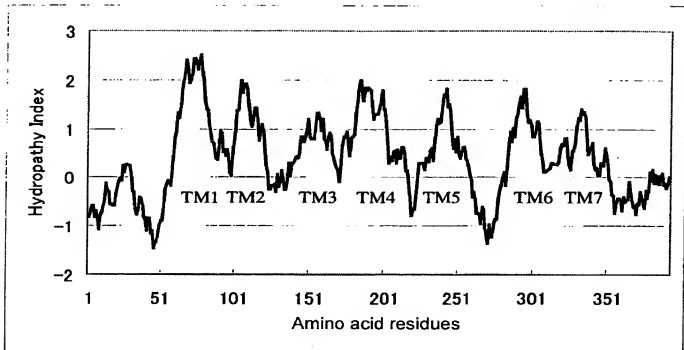


Figure 18

```

GPRv21 -----METTMGFMDDNATNTSTSFSLVNLPHCAHA-TSFPFH
AL121755 -----
AF236082 -----METTVGALGENTDTDTDFSSALDGHEAQT-GSLPFT
U42766 -----MGPIGAEADENQTVEEMKVEQYGP
U76254 -----MGPIGAEADENQTVEEMKVEQYGP
U42389 -----MGPIGAEADENQTVEEMKVEQYGP
U50144 -----MKMGPLGAEADENQTVEEMKVDQFGPG
D86238 -----MVLKMGPVCAEADEN-QTVEVKVEPYGPC
M81490 MYYIAHQGPMLRNEDDNYQEGYFIRPDPA SLIYHTTALPADDEGSNYGYGSTT-TLSGLQ
AF037444 --MSMANSENSTSLFGIKRHADVTGPHSASHDVIDPSNTSVYYDHASNYESVLSTSTLM

##### TM1
GPRv21 FSYSDYDMPL-----DEDEDVTNSR-----TFFAAKIVIGMALVGMVLCGIGNFIF
AL121755 --YGDYDLPW-----DEDEDMTKTR-----TFFAAKIVIGIALAGIMVLCGIGNFIF
AF236082 FSYGDYDMPL-----DEEEDVTNSR-----TFFAAKIVIGMALVGMVLCGIGNFIF
U42766 QTTPRGELVP-----DPEPELIDST-----KLIEVQVVLILAYCSIILLGVI GNSLV
U76254 QTTPRGELVP-----DPEPELIDST-----KLIEVQVVLILAYCSIILLGVI GNSLV
U42389 QTTPRGELVP-----DPEPELIDST-----KLIEVQVVLILAYCSIILLGVI GNSLV
U50144 HTTLPGLAP-----DPEPELIDST-----KLIEVQVVLILAYCSIILLGVI GNSLV
D86238 HTTLPGLAPP-----DPEPELIDST-----KLIEVQVVLILAYCSIILLGVI GNSLV
M81490 FETYNITVMNMFSCDDYDLLSEDMW-----SSAYFKIIVMYLIPIFIFALIGNGTV
AF037444 LKLTDLVTPFNASEPDPSNGSDTGGHAAISEQPMYAKVIVLMYVLIILVAVGGMLLF
* : : : : * : * :
##### TM2 #####
GPRv21 IAAALVRYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYVVVRQLSWEHGHVLCASVNYL
AL121755 IAAALTRYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYVVVRQLSWEHGHVLCASVNYL
AF236082 ITALARYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYVVVRQLSWEHGHVLCASVNYL
U42766 IHVVIFKFSMRTVTNFFIANLAVADLLVNTLCLPFTLYTLMG--EWKMGPVLCPLVPYA
U76254 IHVVIFKFSMRTVTNFFIANLAVADLLVNTLCLPFTLYTLMG--EWKMGPVLCPLVPYA
U42389 IHVVIFKFSMRTVTNFFIANLAVADLLVNTLCLPFTLYTLMG--EWKMGPVLCPLVPYA
U50144 IHVVIFKFSMRTVTNFFIANLAVADLLVNTLCLPFTLYTLMG--EWKMGPVLCPLVPYA
D86238 IHVVIFKFSMRTVTNFFIANLAVADLLVNTLCLPFTLYTLMG--EWKMGPVLCPLVPYA
M81490 CYIYYSTPRMRTVTNFFIASLAIGDILMSFFCEPSSFISLFILN-YWPFGLALCHFVNYI
AF037444 SYVIVMYPKMRSVTNLFLNLNLAISDIKVAVICNPFPAIANLILL-YWPGEFMCQVYVI
: : * : * : : * : * : * : * :
## TM3 ##### TM4 #####
GPRv21 RTVSLYSTNALLAIAIDRYLAIVHPLRPRMKQQTATGLIALVMTVSIILAIIPSAFYFTE
AL121755 RTVSLYSTNALLAIAIDRYLAIVHPLRPRMKQQTASFLIALVMMVSIILAIIPSAFYFTE
AF236082 RTVSLYSTNALLAIAIDRYLAIVHPLRPRMKQQTAAAGLIFLVMSVSIILAIIPSAFYFTE
U42766 QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRI SFLIIGLAWGISALLASPLAIFREY
U76254 QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRI SFLIIGLAWGISALLASPLAIFREY
U42389 QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRI SFLIIGLAWGISALLASPLAIFREY
U50144 QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRI SFLIIGLAWGISALLASPLAIFREY
D86238 QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRI SFLIIGLAWGISALLASPLAIFREY
M81490 QGAVSLVSAYTLVAISIDRYAIAMWLPKPRITKRYATFIAGWFIALATALPIPIVSGL
AF037444 QVVAVFLSAFTLVAMSVDRYVAILKPMRPRLSKRAFAITMATIWIILSASPLPTAITSRV
: : : * : * : : * : : : : * : * :

```

Figure 19

```

      0
***** TM5 *****
GPRv21      TVLVIKVSQ--EKIFCGQINPVDQ--LYYKSYFLIFGIEFVGPVVTMTLCYARISRELW
AL121755    TVLFIKVSQ--EKIFCGQINPVDQ--LYYKSYFLIFGIEFVGPVVTMTLCYARISRELW
AF236082    TVLVIKVSQ--EKIFCGQINPVDQ--FYRYSYLLVFGLEFVGPVVTMTLCYARISRELW
U42766      SLIEIIPDF--EIVACTEKWPGEESKSYGTVYSLSSLLIIVLPLGIIISFSYTRIWSKLL
U76254      SLIEIIPDF--EIVACTEKWPGEESKSYGTVYSLSSLLIIVLPLGIIISFSYTRIWSKLL
U42389      SLIEIIPDF--EIVACTEKWPGEESKSYGTVYSLSSLLIIVLPLGIIISFSYTRIWSKLL
U50144      SLIEIIPDF--EIVACTEKWPGEESKSYGTIYSLSSLLIIVLPLGIIISFSYTRIWSKLL
D86238      SLIEIIPDF--EIVACTEKWPGEESKSYGTVYSLSSLLIIVLPLGIIISFSYTRIWSKLL
M81490      DIPMSPWHTKCEKYICREWWPSSRQ--EYTYTSLSLFALQVVPVLGLIFTYARITIRVW
AF037444    TKQSNSTGL-----CLEHFENDHN--RYIYSIVIMMLQFVPLAVITVTNTHIGYIVW
      * : : : * : : : * : : :

***** TM6 *****
GPRv21      FKA VPG-FQTEQIRKRLCRRTV LVMCILTAYVLCWAPFYGFTIVRDFPPTVFVKEKH
AL121755    FKA VPG-FQTEQIRKRLCRRTV LVMCILTAYVLCWAPFYGFTIVRDFPPTVFVKEKH
AF236082    FKA VPG-FQTEQIRKRTYCRRTV LGLVCLSAVYVLCWAPFYGFTIVRDFPPTVFVKEKH
U42766      NHVSPG-AANDHYHQ--RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE
U76254      SHVSPG-AANDHYHQ--RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE
U42389      NHVSPG-AANDHYHQ--RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE
U50144      NHVSPG-AANDHYHQ--RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE
D86238      NHVSPG-AANDHYHQ--RHKMTKMLVCVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE
M81490      AKRPPGEAETNRDQRMARSKRKMVKMMLTVIVFTCCMLPFNIIQLLLN--DEEFAHNDP
AF037444    IKKTPGEAETDRRMAASKRRLYKMIIVVVIIYAVCNLPVHVITLVGD--HNPDIIYNQPH
      ** : : : : : : : : : : * : : :

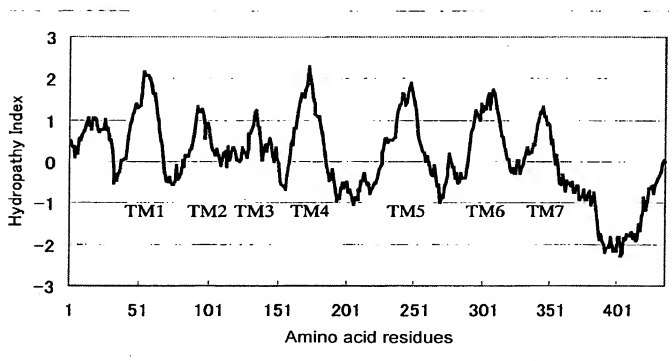
***** TM7 *****
GPRv21      YLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIML-----LHWKASYNGGKS
AL121755    YLTAFYVVECIAMNSMINTVCFVTVKNTNMKYFKKMML-----LHWRSQSGSKS
AF236082    YLTAFYVVECIAMNSMINTLCFVTVNRNTSKYLKRILR-----LQWRASPSGSKA
U42766      YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDLAIHSEV
U76254      YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDLAIHSEV
U42389      YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDLAIHSEV
U50144      YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDLAIHSEV
D86238      YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDLAIHSEV
M81490      LPYVMFAHNLAMSHCCYNPIYCYMNAFRSGFVQLMHRMPLGRNWCCLRSQDORMNAT
AF037444    MNVVMLCAGWLSMASHCYNPFVYFSLSATFRRNRLRMTHACRLKQKR-LRQHLSMRSSRA
      : ** : : : : : : : : : :

GPRv21      S-----ADLDLKTIGM--PATEEVDCIRLK-----
AL121755    S-----ADLDLRTNGV--PTTEEVDCIRLK-----
AF236082    S-----ADLDLRTTGI--PATEEVDCIRLK-----
U42766      SVTFKAK-----KNLEVRKNSG--PNDSFTEATNV-----
U76254      SVTFKAK-----KNLEVRKNSG--PNDSFTEATNV-----
U42389      SVTFKAK-----KNLEVRKNSG--PNDSFTEATNV-----
U50144      SVTFKAK-----KHLQVTKNNG--PNDSFTEATNV-----
D86238      SMTFKAK-----KNLEVKKNNG--PTDSFSEATNV-----
M81490      SGTGPALPLN--RMNSTTTYISARRKPRATSLRANPLSCGETSLR--
AF037444    DAWDRDTEVYGSAESIPSKYSAGSLHSSNRGAKHYNTSSGEQCLKEKLLKGVSNOWYL

```

20/34

Figure 20



21/34

Figure 21

```

**
##### TM1 **
1 MEDLFSPSIL PPAPNISVPI LLGWGLNLTLL GQAPASGPP SRRVRVFLG VILVVAVAGN 60

*****
### ##### TM2 #####
61 TTVLCRLCGG GGPWAGPKRR KMDFLLVQLA LADLYACGGT ALSQLAWELL GEPRAAATGDL 120

*****
@ ##### TM3 ##### ##### TM4 ###
121 ACRFLQLLQA SGRGASAHV VLIALERRRA VRLPHGRPLP ARALAALGWL LALLLALPPA 180

*
#####
### @ ##### TM5
181 FVVRGDSPPSP LPPPPPTSL QPGAPPAARA WPGQRRCHGI FAPLPRWHLQ VYAFYEAVAG 240

*****
#####
241 FVAPVTVLGV ACGHLLSVWW RHRPQAPAAA APWSASPGRA PAPSALPRAK VQSLKMSLLL 300

*****
@ TM6 ##### ##### TM7 #####
301 ALLFVGCELP YFAARLAAAW SSGPAGDWEG EGLSAALRVV AMANSALNPF VYLFFQAGDC 360

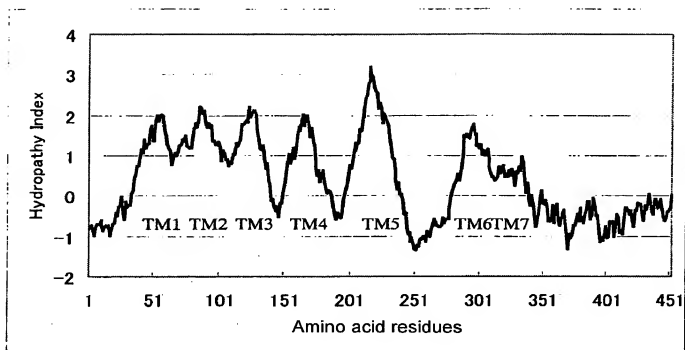
361 RLRRQLRKRL GSLCCAPQGG AEDEEGPRGH QALYRQRWPH PHYHHARREP LDEGGLRPPP 420

421 PRPRPLPCSC ESAF

```

22/34

Figure 22



23/34

Figure 23

```

HSH2R_1
D49783
M32701
U25440
S57565
S73473
M74716
U64032
L41147
GPRv47
D43633

-----
MTFRDL LSVTFEGPRPD I SAGGSGAGGAGAGAGAGD TASSEPAVGGVPGAAGGGGGGS
-----

HSH2R_1
D49783
M32701
U25440
S57565
S73473
M74716
U64032
L41147
GPRv47
D43633

-----
NG-----TASSFCLODSTACKIT-----ITV
MAP-----NG-----TASSFCLODSTACKIT-----ITV
MIS-----NG-----TGSSFCLODPPCRIT-----VSFV
MAF-----NG-----TVPSFCMDFTVYKVT-----ISV
MEP-----NG-----TVNSCCLDSMAKVT-----ISV
MAPWPHKNGS-----LAFWSDAPTLDPASAANTSGLPV-VPW-AAAL
MAPWPHKNGS-----LAFWSDAPTLDPASAANTSGLPV-VPW-AAAL
VVGAGSGEDNRSSAGEPGGAGGGGGE-----VNGTAAGVGLVYSQASVGC-----VGV
MVP-----EPGPT-----ANSTPAWGAGPPSAPGGSG-----WVAA
MESSPI PQSSGNSS TLGRVPQTGPSTASGVPEVGLRDV-ASESVALF
MMADKTS PMITSDHSI SNFSTGLFGPHTVPPDVGVVTS SQSQMKDLGFLG

### TM1 #####
HSH2R_1
D49783
M32701
U25440
S57565
S73473
M74716
U64032
L41147
GPRv47
D43633

VLA V L I L I T Y A G N V V Y C L A V G L N R R L N R L T N C F I V S L A I T D L L G L L V L P F S A I Y Q L S C K
V L A V L I L I T Y A G N V V Y C L A V G L N R R L N R L T N C F I V S L A I T D L L G L L V L P F S A I Y Q L S C K
V L T V L I L I T Y A G N V V Y C L A V G L N R R L N R L T N C F I V S L A I T D L L G L L V L P F S A F Y Q L S C R
I L I I L I L T Y A G N V V Y C L A V G L N R R L N R L T N C F I V S L A V T D L L G L L V L P F S A I Y Q L S C K
V L T T L I L I T Y A G N V V Y C L A V S L N R R L N R L T N C F I V S L A A T D L L G L L V L P F S A I Y Q L S F T
A G A L L A L A T V G G N L L V I T A I A R T P R L Q T I T N V F V T S L A T A D L V G L L V M P P G A T L A L T G H
A G A L L A L A T V G G N L L V I T A I A R T P R L Q T I T N V F V T S L A T A D L V G L L V M P P G A T L A L T G H
F L A A F I L T A V A G N L L I L S V A C N R H L Q T V T N Y F I V N L A V A D L L S A T V L P F S A M E V L G F
A L C V I A L T A A A N S L L I A L I C T P A L R N T S N F F L V S L F T S D L M V G L V M P P A M L N A L Y G R
F M L L D L T A V A G N A A V M A V I A K T P A L R K F V F V F H L C L V D L L A A L T M P L A M L S S A L F D H
C M V T L N L I A L L A N T G V M V A I A R A P H L K K F A V C H L C A V D V L C A I L L M P L G I I S S P F F G

. : . * : : * . : :

### TM3 #####
HSH2R_1
D49783
M32701
U25440
S57565
S73473
M74716
U64032
L41147
GPRv47
D43633

W S F G K V F C N I Y T S L D V M L C T A S I L N L F M I S L D R Y C A V M D P L R Y P V L T P R V A I S L V L I W
W S F G K V F C N I Y T S L D V M L C T A S I L N L F M I S L D R Y C A V M D P L R Y P V L T P R V A I S L V L I W
W S F G K V F C N I Y T S L D V M L C T A S I L N L F M I S L D R Y C A V T D P L R Y P V L T P R V A V S L V L I W
W S F G K V F C N I Y T S L D V M L C T A S I L N L F M I S L D R Y C A V T D P L R Y P V L T P R V A I S L V L I W
W S F G H V F C N I Y T S L D V M L C T A S I L N L F M I S L D R Y C A V T D P L R Y P V L T P R V A I S L V L I W
W P L G A T G C E L W T S D V L C V T A S I E T L C A L A V D R Y L A V T N P L R Y G T L V T K R R A R A A V V L V W
W P L G A T G C E L W T S D V L C V T A S I E T L C A L A V D R Y L A V T N P L R Y G T L V T K R R A R A A V V L V W
W A F G R A F C D V W A A V D V L C C T A S I L S L C T I S V D R Y V G V R H S L K Y P A I M T E R K A A A I L A L L
W V L A R G L C L L W A T A F D M C C S A S I L N L C L I S L D R Y L L I S P L R Y K L R M T P R A L A L V L G A N
A L F G E V A C R L Y L F L S V C F V S L A I L S V A I N V E R Y Y V V H P M R Y E V K M T L G L V A S V L G V W
V V F T I L E C Q V Y I F L N V F L I W L S I L T I A I S V E R Y F Y I V H P M R Y E V K M T I N L V I G M L L I W

: * : . * : : : : : : : : : : : : : : :

```

Figure 24

```

#####
HSH2R_1 VISITLSFLSIHLGWN---SRNETSKGNHTTSKCN-----VQVNEVYGLVDGLVTFFYLPLLMICI
D49783 VISITLSFLSIHLGWN---SRNETSKGNHTTSKCK-----VQVNEVYGLVDGLVTFFYLPLLMICI
M32701 VISITLSFLSIHLGWN---SRNETSSFNHTIPKCK-----VQVNLVYGLVDGLVTFFYLPLLMICI
U25440 VISITLSFLSIHLGWN---SRNETSKNDITVCK-----VQVNEVYGLVDGLVTFFYLPLLMICI
S57565 VISITLSFLSIHLGWN---SRNGTRGDN-DTFCK-----VQVNEVYGLVDGLVTFFYLPLLMICI
S73473 IVSATVVSFAPIMSQWVRVGADAEAEQCHSNPRCCS-----FASNMPYALLSSVSFYLLPLLMVLF
M74716 IVSATVVSFAPIMSQWVRVGADAEAEQCHSNPRCCS-----FASNMPYALLSSVSFYLLPLLMVLF
U64032 AVALLVVS-MGPLLGMK-----EPVPPD--ERFC-----GITEEVGYAVFSSCSFYLLPMVAIVV
L41147 SLAALASFLPLLLGMH-----ELGHARPPVPGQC-----RLLASLFPVLVASGLTFFLPSGAICF
GPRv47 VKALAMASVYPLGRVS--WEEGAPSVPPG-----CSLQWHSAYCQLFVVVFAVLYLLPLLLIIV
D43633 FKSLLLA-LVTLFGWPPYGHQSSIAASH-----CSLHSHSRLRGVFAVLCFICFLAPVYVIFS
: : : * : : * * :

*
HSH2R_1 TYRIFRVARDAQKRID-HIS-----SWKAATIR-----
D49783 TYRIFKVARDAQKRIN-HIS-----SWKAATIR-----
M32701 TYRIFKIARDQAKRIH-HMG-----SWKAATIG-----
U25440 TYRIFKFIAREQARRIN-HIG-----SWKAATIR-----
S57565 TYRIFKFIAREQAKRIN-HIS-----SWKAATIR-----
S73473 VYARVFVYAKRQRRLRLRELGRFPPEESPRSPSPSPATVGTPTAS-----DGVPSGCR
M74716 VYARVFVYAKRQRFRYRRELGRFPPEESPRSPSPSPATVGTPTAS-----DGVPSGCR
U64032 MYCRVYVYARSTTRLEAGVKRERKASEVVLRIHCRGAASGADGAPGTRGAKGHTFRSS
L41147 TYCRILLAARKQAVQVASTTGT-----MASQASSETLQVPRTP--R--PGVESAD
GPRv47 VYCSMFVRVARVAAMQHGLPTWETP-----RQRSELSLR--S--TMTVSSGA
D43633 VYSAYVKVARSAALQVPAVPTWADAS-----PAKORDSDINSQTT-----IITRTLTP
* : * : :

##### TM6 #####
HSH2R_1 -----EHRATVTLAAYMGAFIICWFYFATFVYRGLRGDDAINEMLEAIVLWLG
D49783 -----EHKATVTLAAYMGAFIICWFYFATFVYRGLRGDDAINEVLEAIVLWLG
M32701 -----EHRATVTLAAYMGAFIICWFYFATFVYRGLRGDDAINEAEAVVLWLG
U25440 -----EHKATVTLAAYMGAFIICWFYFATFVYRGLRGDDAINEVEFVVLWLG
S57565 -----EHRATVTLAAYMGAFIICWFYFATFVYRGLRGDDAINEVEGIVLWLG
S73473 RPARLLPLG-EHRALRTLGLIGIFSLCWLFFLANVLRALVGPSPVPSGVIALNWLG
M74716 RPARLLPLG-EHRALRTLGLIGIFSLCWLFFLANVLRALVGPSPVPSGVIALNWLG
U64032 LSVRLKFSREKKAAKTLAIVGVGVLCWFPPFFVPLGSLFPOLKPSGEVFKYIFWLGY
L41147 RRLATKHSRKALKASLTGLIGLGMFFYTLPPFFVANI VQAVC--DCISPLGFDVTLWLG
GPRv47 PQTTHRTFGGKAAVLLAVGGQFLCWLPLYFSHLYALSAGPISTGGQVESVTVIIGY
D43633 QRLSPERAFSGGKAALTAFIVGQFLVCLPFFIFHLQWSLTGSMSKSPGDEEAVNWLAY
: * : * : * : * : : * : *

TM7 #####
HSH2R_1 ANSALNPILYAALNRDFTGYQQLFCCLLRANRNSHKTSLSRNASQLSRQTOSREPR---Q
D49783 ANSALNPILYAALNRDFTGYQQLFCCLLRANRNSHKTSLSRNASQLSRQTOSREPR---Q
M32701 ANSALNPILYATLNRDFTAYQQLFCRCPASHNAQETSLSRNASQLSRQTSREPR---R
U25440 ANSALNPILYAALNRDFTAYQQLFCCLASHNSHETSLSRLNNSQLNRSGQREPR---W
S57565 ANSALNPILYAALNRDFTAYQQLFHCCKFASHNSHKTSLSRLNNSQLNRSGREGR---W
S73473 ANSAFNPLIYCR--SPDFRDAFRLL--CSYGGRGPEEP--RVVTFPASPVASR---
M74716 ANSAFNPLIYCR--SPDFRDAFRLL--CSYGGRGPEEP--RVVTFPASPVASR---
U64032 FNSCVNPLIYPCSSREFKRAFLRLRCQCRRRRRRLPWRVYGHNWRASAGGPHPCDL
L41147 CSTMNPNIYPLFMRODKRALGRFLPCPRCPRERQAS--LASPSLRTSHSGPRPLS--N
GPRv47 FCFSTNPFYGLCLNRQIRGELSKQFVCFKPAPEEELRLPSREGSIENFLQ---F
D43633 SSFAVNPISYGLLNRQIRDELVKFRRCCTVQPVEIGP--SSLEGSFQENFLQ---F
* : * : : * :

```


Figure 25

HSH2R_1	QEEKPLKLQVWSGTEVT-----
D49783	QEEKPLKLQVWSGTEVTAPQGATR-----
M32701	QEEKPLKLQVWSGTEVTAPQGATR-----
U25440	QEDKPLNLQVWSGTEVTAPQGATNR-----
S57565	QEEKPLKLQVWSGTELTHPQGNPIR-----
S73473	QNS-PLNR--FDGYEGERP-FPT-----
M74716	QNS-PLNR--FDGYEGERP-FPT-----
U64032	SAGAALPGAALALTAAPAPSSAAAPGQAAAGAGRRKPPCAFREWRLLGPLRRPTTQLRAK
L41147	QQVLPLPLPPDSDSDDAGSGGSSGLRLTAQLLLPGEATQDPLPTRAAAAVNFFNIDPA
GPRv47	LQGTGCPSESWSRPLSPKQEPFAVDRI PGQIAEETSEFLEQQLTSDIIMSDSYLRPA
D43633	IQRTSSSSSETHPSFANSNP-RNMENQAHKI PGQIPPEQA-----
HSH2R_1	-----
D49783	-----
M32701	-----
U25440	-----
S57565	-----
S73473	-----
M74716	-----
U64032	YSSLSHKI RAGGAQRAEAACALRSEVEAVALSVARDVAEDNTCQAYELADYRNLRETDI
L41147	EPELRPHPLGIPTN-----
GPRv47	ASPRLES-----
D43633	-----

26/34

Figure 26

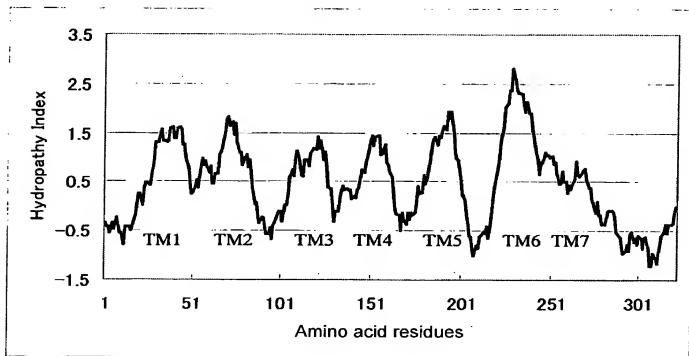


Figure 27

```

***** TM1 #
GPRv51 -----MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMA
M35297 MAGNCSEAHSTNQNKWCPGMSEAELYSRGLTIEQIATLPPPAVTNYIFLLCLCGLV
          ** . * : **** . *.. : :: *****

***** TM2 *****
GPRv51 GNSMWIVLLGFRMRHPFCIYILNLAAADLLFLFMASTLSLETQLPVN-TTDKVHELMK
M35297 GNGLVLFNFFGFSIKRTPFISIYFLHLASADGIYLFASKAVIALLNMGTFLGSFPDYVRVSRR
          **: *: **: ** :*:***: :*** * : : .. * *: : :

***** TM3 ***** ***** TM4 *****
GPRv51 RLMFYATTVGLSLLTAISTQRCLSVLPFIWFKCHRPRLHSAWCGLLWTLCLLMNGLTSS
M35297 IVGLCTFFAGVSLPAPISIERCVSIFPMWYWRRRPKRLSAGVCALLWLILLSFLTYSIHMY
          : : .*:***:**:***:*: :***:*** **.* *.: : .

# ***** TM5 *****
GPRv51 FCSKFLKFNE-DRCFRVDVMQAALIMGVLPVNTLSLTLFVVYRRSSSQWRRQPTRLFV
M35297 FCMFLGHEASGTACLNDISLGILLFFLCPLMVLPCLAILHVCECRARRRQRS-AKLNH
          ** : : . *:*: . *: : *:*.~*:~* . : : *. : ~*

***** TM6 ***** ***** TM7 *****
GPRv51 VVLASLVFLICSLPSIYWFWLYLWSLPPMQVLCFSLRSLSVSSSANPIYVFLVGS
M35297 VVLAIVSVFLVSSIYLIGIDWFLFWVFQIP---APPFEYVTDLCICINSSAKPIVYFLAGR
          *** * **:.*: * * **: : : * : : : * . : .***:~*:~*

GPRv51 RRSRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNEMGA-----
M35297 DKSQRLMEP-LRVVFQALRDGAEPGDAASTPNVTVMEMQCPSGNAS
          :*:~* * *:~*:~* ** ..... * ~*

```

28/34

Figure 28

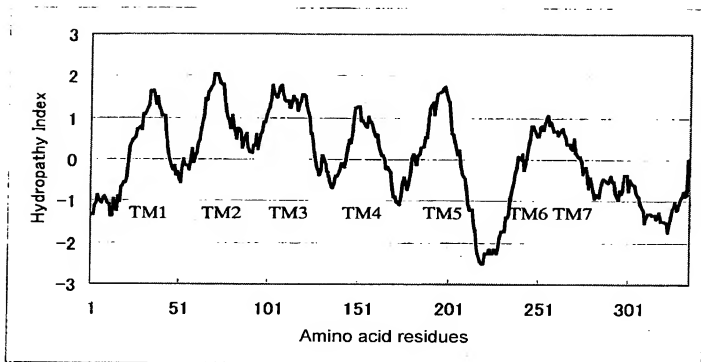


Figure 29

```

Y14705 -----MTSAESLFTSLGSPSSGDDCRFNEEFFKILPLMSYAVFVLGLAL
AJ277752 -----MTSADSLFTSLGSPSSGDDCKFNEEFFKILPLSYAVFVLGLAL
AF031897 -----MDAPVRWMSLAPWPTPTPTFWLGGNTAAAEAKCYFNEEFFKILPLSYGIVFYVGLPL
X99953 -----MTEDIMATSYPTFLTTPPLPKMLMLNLTDEDICVFDEGDEHILPPSYSAVFMVGLPL
AF069555 -----MSMANFTA-----NSCTGQEEFKVQLPLVYSVFLGLGLPL
X98283 -----MSMANFTG-----NSCTHEEFKQVLLPLVYSVFLGLGLPL
D63665 -----MEKDRNGTIQAPGLPP-----TLTCVYREDFKRLLLPPVYSVFLVGLPL
GPRv71 -----MEKYDMNTSQ-----GLQCSEKYQKYLAYSIIIFILGLPL
* : * : * : * : * : * :

#####
##### TM2 #####
#####
Y14705 -----NAPTLWLFLFLRLRPWDATATYMFHALSDTLVYLSLPTLVVYAAHNNHWPFGTCLCKFVR
AJ277752 -----NAPTLWLFLFLRLRPWDATATYMFHALSDTLVYLSLPTLVVYAAHNNHWPFGTCKFKFVR
AF031897 -----NSWANNIFVFSRMRPWNAATTYMFENLAI SDTLVYFSLPTLVVYAADRNHWPFGVKCFIVR
X99953 -----NIAAMWIFIAKMRPWNPPTTYMFENLAI SDTLVYFSLPTLVVYAADRNHWPFGVKCFIVR
AF069555 -----NAVYIGIILWARKALTRTIYMLNLADTLVYCSLPLIINYTKQDYWPFQDGTCKFVR
X98283 -----NAVYIGIILWARKALTRTIYMLNLADTLVYCSLPLIINYTKQDYWPFQDGTCKFVR
D63665 -----NVCGIAIQCARSLRTLSRAYVTLNLALADYLAACSPLIINYARGDHPFGDLACLRVL
GPRv71 -----NGTVLWHFNGQTKRWSCATLYLVNLVADLLV-LPFLIITYSLDDRNPFGELCKLKV
* : * : * : * : * : * :

#####
##### TM3 #####
#####
Y14705 -----FLFYWNLYCSVFLFTICSVHRYMGICHLPAIRIWRGRPR-FASLLCLGVNLVYAGCLVPNL
AJ277752 -----FLFYWNLYCSVFLFTICSVHRYMGICHLPAIRIWRGRPR-FAGLLCLGVNLVYAGCLVPNL
AF031897 -----FLFYANLYSSILFLFTICSVHRYMGICHPIRSLKWWKTK-HARILCGVNLVYIGLIPNL
X99953 -----FLFYANLYSSILFLFTICSVHRYGVCHPIITSLRRNNAH-HAYVILCAQLWNLVYTLQVNLPL
AF069555 -----FQFYTNLHSGIILFLFTICISVQRYMGICPLASHWHKKKGKGLVTLCAAVWFIIVIAQCLPTF
X98283 -----FQFYTNLHSGIILFLFTICISVQRYMGICPLASHWHKKKGKGLVTLCAAVWFIIVIAQCLPTF
D63665 -----FLFYANLYSSILFLFTICISVQRYMGICPLAPHWKRGGRRAAWVLTGCVANWFIIVIAQCLPTF
GPRv71 -----FLFYANLYSGIILLTICISVHQFLGVCHPCLSPYRTRR-HAWLGSTSTWALVVLQQLPTF
* * * : * : * : * : * : * : * :

#####
##### TM4 #####
#####
Y14705 -----FLFYWNLYCSVFLFTICSVHRYMGICHLPAIRIWRGRPR-FASLLCLGVNLVYAGCLVPNL
AJ277752 -----FLFYWNLYCSVFLFTICSVHRYMGICHLPAIRIWRGRPR-FAGLLCLGVNLVYAGCLVPNL
AF031897 -----FLFYANLYSSILFLFTICSVHRYMGICHPIRSLKWWKTK-HARILCGVNLVYIGLIPNL
X99953 -----FLFYANLYSSILFLFTICSVHRYGVCHPIITSLRRNNAH-HAYVILCAQLWNLVYTLQVNLPL
AF069555 -----FQFYTNLHSGIILFLFTICISVQRYMGICPLASHWHKKKGKGLVTLCAAVWFIIVIAQCLPTF
X98283 -----FQFYTNLHSGIILFLFTICISVQRYMGICPLASHWHKKKGKGLVTLCAAVWFIIVIAQCLPTF
D63665 -----FLFYANLYSSILFLFTICISVQRYMGICPLAPHWKRGGRRAAWVLTGCVANWFIIVIAQCLPTF
GPRv71 -----FLFYANLYSGIILLTICISVHQFLGVCHPCLSPYRTRR-HAWLGSTSTWALVVLQQLPTF
* * * : * : * : * : * : * : * :

#####
##### TM5 #####
#####
Y14705 -----FJFTVNTANGTILCHDHTLPEEFDHVYFSSAVMWLVFLGLPFLITLVCYGLMARRLYRPL
AJ277752 -----FJFTVNTANGTILCHDHTLPEEFDHVYFSSAVMWLVFLGLPFLITLVCYGLMARRLYRPL
AF031897 -----IFVTTNSKDNSTLCHDTTKPEFDHVFHYHSSIMALLGFPFLIVTCVGLMAKRLCKRS
X99953 -----IFVTVSPKWNITICHTIRPEDFARVYEYGAIMCLLGPICLIAGCYGLMTRELKMP
AF069555 -----VFASSTQNRNTVCDYLSPPDRASFYEGTITLTITGFLPFLAIACYCSMARILCQD
X98283 -----VFASSTQNRNTVCDYLSPPDRSTSYFPGYITLTITGFLPFLAIACYCSMARILCQD
D63665 -----VFAATGICQRNRTVCDYLSPPITLSTRLYPCYGMALVITLYVRSSPTLCPPTLQAFQAI
GPRv71 -----AFSHTDYINGQMUYWDITSQENFDRIFAYGIVLTSGLFSLGLGHGFVLTGDGEPDQARG
* : * : * : * : * : * :

#####
##### TM6 #####
#####
Y14705 -----PGACQS-----SRLRSRLRTIAVVLTVFAVCFVPFHIITRTIYYQAR-LLQADCHVLNIVNV
AJ277752 -----PGAGQS-----SRLRSRLRTIAVVLTVFAVCFVPFHIITRTIYYAR-LLNAECVHLNIVNV
AF031897 -----FSPSPRPVYSKKRSIKMIILVTVAFICVFPFHIITRTIYYAR-FYQACQTLNIINFT
X99953 -----VSGNQQTLPYSKKRSIKTIIFVMIAFACFMPFHIITRTIYYAR-LLGKICYALNIVNVT
AF069555 -----ELIGLAVH-KKKDKAVRMIILVIVISFFPHLTITLYIVRSSPTLCPPTLQAFQAI
X98283 -----ELIGLAVH-KKKDKAVRMIILVIVISFFPHLTITLYIVRSSPTLCPPTLQAFQAI
D63665 -----PGAPVYAQ-ERRSKAARMVAWVAVFISFLPFIITKTAFLVRSRTPGCVSPTLEFAAA
GPRv71 -----EPHEDRQHSFSQVPHDPHTGVWPLHPLFCALPHYSLPLPHLLSFAFSGPLPADGSCQGLQ

```

30/34

Figure 30

```
##### TM7 #####
Y14705      YKVTRPLASANSCLDPVLYLFTGDKYRNQLQQLCRGSK--PKPR-----TAASSL
AJ277752    YKVTRPLASANSCLDPVLYLFTGDKYRNQLQQLCRGST--PKRR-----TTASSL
AF031897    YK1TRPLASINSCLDPILYFMAGDKYRGRLRGAQAQR--P-R-----PVPTSL
X99953      YKVTRPLASANSCLDPILYFLANDRYRRRLIRTVRRRSSVPNRRCMHTNHPQTEPHMTAG
AF069555    YKCTRPFASMNSVLDPILFYFTQQRKFRESTRYLLDKMS-----SKWRHD
X98283      YKCTRPFASMNSVLDPILFYFTQQRKFRESTRYLLDKMS-----SKWRQD
D63665      YKCTRPFASANSVLDPILFYFTQQKFRRQPHDLLQKLT-----AKWQRQ
GPRv71      DMEASGECEQLPQPSVLVSFKGGKNRVRLQLKLQKNKLG-----EHPAGRK
           : .. . .*:~

Y14705      ALVTLHEESISRWADTHQDSTFSAYEGDRL-----
AJ277752    ALVTLHEESISRWADTHQDSIFPAYEGDRL-----
AF031897    LALVSPSVDSSVVGSCCNSE---SRGMGTVMVSRGGQ-----
X99953      PLPVISAEEIPSNGSWVRDENGEGSREHRVEWTDKEINQMMNRRSTIKRSTDKNDMKE
AF069555    HCITYGS-----
X98283      HCSYGS-----
D63665      RV-----
GPRv71      RCPGLNRSG-----

Y14705      -----
AJ277752    -----
AF031897    -----
X99953      NRHGENYLPYVEVVEKEDYETKRENKTTQSSKTNAEQDELQTQIDSRLLKRGKWLSSK
AF069555    -----
X98283      -----
D63665      -----
GPRv71      -----

Y14705      -----
AJ277752    -----
AF031897    -----
X99953      KGAAQENEGKHMEPSFEGETSTWNLLTPKMYGKKDRLAKNVEEVGYGKEKELQNFPA
AF069555    -----
X98283      -----
D63665      -----
GPRv71      -----
```

31/34

Figure 31

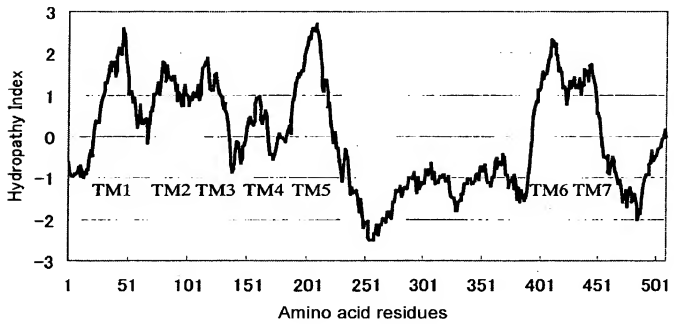


Figure 32

```
U03866 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
L31774 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
D25235 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
D32202 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
D32201 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
AF013261 -----MVFLSGNAS-----DSSNCTQPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
U81982 -----MVFLSGNAS-----DSSNCTHPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
U07126 -----MVLLENAS-----EGSNCTHPPAP-----VNISKAILLGVILGGLILFGVLGNILV  
S71323 MVPVLNDNMTPSSVTLL--NCNSCHVLAPE-----LNTVKAVLVGMVLGIIFLGVGIGNILV  
D63859 --MTPSSVTLL--NCNSCHVLAPE-----LNTVKAVLVGMVLGIIFLGVGIGNILV  
AF091890 ---MSLNSSLKCKELSLNTEEEGG---EGGVIITQFIAIIVITI FVCLGNILV  
GPRv72 ----MTSTCTNST----RESNSSHTCMPLSKMPI SLAHGITRSTVLVI FLAASFVGNIVL  
  
              :      * * :                     :               :      * *: :  
  
###          ##### TM2 ##### @#####  
U03866 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
L31774 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
D25235 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
D32202 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
D32201 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
AF013261 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADV  
U81982 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAADV  
U07126 ILSVACHRHLSHYTHYIYNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAADV  
S71323 ILSVACHRHQLTQTYTFYINLAVADLLSSTVLPFSAIFEILD RVFGRVFCNIWAADV  
D63859 IVTVLKYSYLLTL SNKFVSFLTSLNFFLSVLFPVFTSIIRREWI FGVMWCNFSAALLYL  
AF091890 ALVLQRKPQLLQTNRFI FNLLVTDLQI SLVA PWVVATSVPLFWPLNSHFCTALVSLTH  
GPRv72  
  
# TM3 #####                     ##### TM4 #####  
U03866 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
L31774 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
D25235 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
D32202 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
D32201 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
AF013261 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGLMALLCVNALSLVISIGPLFGWR-  
U81982 LCCTASIMGLCISI IDRYIGVSYPLRYPTIVTORRGRLALLCVNALSLVISIGPLFGWR-  
U07126 LCCTASIMGLCI ISIDRYIGVSYPLRYPTIVTORRGRLALLCVNALSLVISIGPLFGWR-  
S71323 LCCTASIMSCVISIDRYIGVSYPLRYPIATRKRALLAVMLLVLSVISIGPLFGWK-  
D63859 LCCTASIMSLCWSVDRIYGVSYPRLPYAITMKRRALLAVMLLVLSVISIGPLFGWK-  
AF091890 LISSASM LTLGVAI DRYAYVLPMPVPMKI TGNRAVMALYIWLHSI GCLPPLFGWSS  
GPRv72 LFAPASVNTIVVVSVDRLSI IHLSPTSXKMTRQGRLLYGTWIVA ILQTSPTPLGCWGQ  
* . * : : : : : * : : * : : * : : * : : * : : *
```


Figure 33

```

##### TM5 #####
U03866 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
L31774 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
D25235 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
D32202 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
D32201 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
AF013261 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
U81982 QPAPDDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
U07126 QPAPEDETICQINE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---S
D63859 EPAPEDETVCKITE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---E
AF091890 EPAPEDETVCKITE--EPGYVLFSAFGSYFLPLAIILVMYCRVYVAKRESRGLK---E
GPRv72 VEFDEFKMMCVAAWHREPGYAFWQIWCALFPFLVMLVCYGFIFRVARVKARKVH---C
AAFDERNALCSMIWGASPSYITLSVVSFIVPLIVMIAACYSVVFCAARRQHALLVYVNRH
: : * . * . : : * : : . * : : * : :

#####
U03866 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
L31774 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
D25235 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
D32202 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
D32201 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
AF013261 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLKFSREKKAATLGI VVG-
U81982 GLKTDKSDSEQVTLRIHRKNAPAGGSGVASAKNKTTHFSVRLKFSREKKAATLGI VVG-
U07126 GLKTDKSDSEQVTLRIHRKNVPAEGGVSASAKNKTTHFSVRLKFSREKKAATLGI VVG-
D63859 GQKIEKSDSEQVILRMHRCNTTVSED--EALRSRTHFALRLKFSREKKAATLGI VVG-
AF091890 GTVVI VEEDAQRTG--RKNSTSTS--SSGSRNAFQGVVYANQCK--ALITILVVLG-
GPRv72 SLEVRVKDCVENEDEGAKEEFQD--ESEFRHQHEGVKAKEGRMEAKDGSLLAKEGS
. : : : : : : : : : : *

##### TM6 ##### ##### TM7
U03866 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
L31774 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
D25235 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
D32202 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
D32201 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
AF013261 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
U81982 ----CFVLCWLP----FFLVMPIGSFFPD--FKPPETVFKIVFWLGYLNSCIN----
U07126 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
D63859 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
AF091890 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
GPRv72 ----CFVLCWLP----FFLVMPIGSFFPD--FKPSETVFKIVFWLGYLNSCIN----
TGTSESSVEARGSEEVRESSTVASDGSMEGKEGSKTVEENSMKADKGRTEVQNCSIDLGE
: : : : : * : : : : :

```

Figure 34

```

#####
U03866 -PIIYPCSSQEFK---KAFQNVLR IQCLCRKQSSKH---ALGYT-LHPPSQAVEGQHK-
L31774 -PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D25235 -PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D32202 -PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D32201 -PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
AF013261 -PIIYPCSSQEFK---KAFQNVLR IQCLCRKQSSKH---ALGYT-LHPPSQAVEGQHK-
U81982 -PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHAPSQALEGQHK-
U07126 -PIIYPCSSQEFK---KAFQNVLR IQCLRRRQSSKH---ALGYT-LHPPSQALEGQHK-
S71323 -PIIYLCSNQEFK---KAFQSVLLGVHCLRMTPTRAHHHHL SVGQSQTGQHS LT I SLOSKG
D63859 -PIIYLCSNQEFK---KAFQSVLLGVHCLRMTPTRAHHHHL SVGQSQTGQHS LT I SLOSKG
AF091890 -PLIYGLWN---KTVRKELLCMGCFGDYRYREP---FVQR-QRTSRLFSI SNR
GPRv72 DMEFGEDDINFSEDDVEAVNI PESLPPSRNNSNPN---PLPRCYCKAAKVIFIIIFS
: : : : :

U03866 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARVRSKS
L31774 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARVRSKS
D25235 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARVRSKS
D32202 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARTKSRS
D32201 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARGHTPM
AF013261 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARRGMDC
U81982 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVSKDQS---SCTTARRGMDC
U07126 DMVRI PVGSRETFYRI SKTDG---VCEWKFSSMPRGSARI TVPKDQS---ACTTARVRSKS
S71323 APCRLSPSSVALSRT PSSRD---SREWRVFGGPI NSG---PGPTEAG---RAKVAKLCNKS
D63859 APCRLSPSSVALSRT PSSRD---SREWRVFGGPI NSG---PGPTEAG---RAKVAKLCNKS
AF091890 -ITDLGLSPHLTALMAG---GQPLGHS---SSTGDTG---FSCSQDSGN-
GPRv72 YVLSGLPGYCLAVLAVWVDVETQVPQWVIT I I WLFLLQCCIHPYVYGVMHKT IKKEIQD
: : : : :

U03866 FLQVCCCVGPS-TPSLDKN---HQVPTIKVHT I SLSengeEV-----
L31774 FLQVCCCVGPS-TPSLDKN---HQVPTIKVHT I SLSengeEV-----
D25235 FLEVCCCVGPS-TPSLDKN---HQVPTIKVHT I SLSengeEV-----
D32202 VTRLECSG---MILAHCN---LRLPGSROS PASASQAAGTTGDVPPGRRHQAQLIFVFLV
D32201 T-----
AF013261 RYFTKNCR---EHIKHVN---FMMPWRKGLEC-----
U81982 FLQVCCCVGPS-TPMPGEN---HQVPTIKIHT I SLSengeEV-----
U07126 FLQVCCCVGPS-APRPEEN---HQVPTIKIHT I SLSengeEV-----
S71323 LHRTCCCLIRARTPTQDPAPLGDLPTIKIHQLSLSEKGESV-----
D63859 LHRTCCCLIRARTPTQDPAPLGDLPTIKIHQLSLSEKGESV-----
AF091890 -LRAL-----
GPRv72 MLKKFFCKEK---PPKEDSH---PDLPGTEGGTEGI VPSYDSATFP-----

U03866 -----
L31774 -----
D25235 -----
D32202 ETGFHHVGGDDLLD LLS
D32201 -----
AF013261 -----
U81982 -----
U07126 -----
S71323 -----
D63859 -----
AF091890 -----
GPRv72 -----

```